SFB 680
Molecular Basis of Evolutionary Innovations

SFB 680 / 20th Seminar Day
Mini Symposium on viral Evolution
December 3 and 4, 2015

Abstracts

Georgii Bazykin, Kharkevitch Institute, Moscow

The role of epistasis in evolution of influenza A

The amino acid residues of influenza proteins interact, and these interactions shape viral evolution in ways that may be important for prediction of antigenic drift or emergence of drug resistance. Such interactions can be efficiently inferred from viral phylogenetic data. I will tell about our work in this direction. If a substitution at site A is systematically followed by a substitution at site B, these sites likely interact. This approach may be used to infer both intra-protein and inter-protein interactions; in the latter case, however, situation is complicated by reassortments which lead to incongruencies between phylogenies of different viral proteins. Finally, reassortment events themselves cause bursts of subsequent amino acid substitutions, probably due to adaptation of proteins to a new genetic environment that they find themselves in.

William Harvey and Richard Reeve, Institute of Biodiversity Animal Health and Comparative Medicine, Glasgow University

Identifying genetic determinants of antigenic differences among RNA viruses

Genetic and antigenic variants continue to emerge within each of the human influenza A subtypes and within each of the seven foot-and-mouth disease virus serotypes. Antigenic variation has important implications for the epidemic potential of emerging strains, outbreak severity and vaccine selection. In this talk, I'll discuss a direct integration of amino acid sequence and antigenic data that makes quantitative estimates of the antigenic impact of specific substitutions. Our results provide a detailed explanation of the relationship between molecular and antigenic evolution, which increases our understanding of epitope conformation and of the interaction between antigenic proteins and the host immune system. Quantifying the antigenic impact of amino acid changes also allows us to accurately predict antigenic phenotype from sequence data. This could aid the targeting of antigenic assays and hasten the identification of emergent antigenic variants.

Marta Luksza, Institute for Advanced Study, Princeton

Epidemiological and evolutionary analysis of the 2014 Ebola virus outbreak

The 2014 epidemic of the Ebola virus is governed by a genetically diverse viral population. In the early Sierra Leone outbreak, a recent study has identified new mutations that generate genetically distinct sequence clades. Here we find evidence that major Sierra Leone clades have systematic differences in growth rate and reproduction number. If this growth heterogeneity remains stable, it will generate major shifts in clade frequencies and influence the overall epidemic dynamics on time scales within the current outbreak. Our method is based on simple summary statistics of clade growth, which can be inferred from genealogical trees with an underlying clade-specific birth-death model of the infection dynamics. This method can be used to perform realtime tracking of an evolving epidemic and

Simone Pompei, Institute for Theoretical Physics, University of Cologne

Analysis of epistasis in the haemagglutinin protein of human influenza

Abstract: The seasonal influenza A (H3N2) virus undergoes rapid evolution to escape human immunity. Adaptive changes occur through a high supply of beneficial mutations, in a strong clonal interference regime. At the same time, epistatic effects on pathogen fitness are expected to play an important role in the immune-escape. However, hitchhiking and selective sweeps can confound linkage disequilibrium, as well as closely timed substitutions, as indicators of epistasis.
Here, we present a new method to analyze epistatic effects which is suitable for systems evolving under strong clonal interference. We apply this method to hemagglutinin (HA), the surface protein of the human influenza virus primary involved in the response to the immune system.

Mara Villa, Institute for Theoretical Physics, University of Cologne

Detection of reassortment in the evolution of influenza virus

The process of reassortment, namely the mutual mixing of coinfecting pathogens segments during replication in the host cell, is known to play a relevant role in the evolution of segmented viruses. The introduction in the viral population of variants that share segments coming from different evolutionary backgrounds can lead to relevant fitness advantage and, on the other hand, acts as a randomizing factor in the picture of coevolution of the entire genome.
Here we propose a new phylogenetic method to detect reassortment occurring in fast evolving systems and we apply it to H3N2 human influenza A virus, focusing in particular in mutual exchange of hemagglutinin and neuraminidase proteins.